

**IN THE CLAIMS:**

Please cancel claims 10, 13-15 without prejudice or disclaimer, and amend claims 1, 3, 5-6 and 12 as follows:

1. (Currently Amended) A method for assembling nucleic acid base sequences comprising the steps of:

providing a plurality of nucleic acid base sequences;

moving a window of a fixed length along a first nucleic acid base sequence of the plurality of nucleic acid base sequences to define a first fixed-length partial sequence and simultaneously searching for a second nucleic acid base sequence among the plurality of nucleic acid base sequences which has a second fixed-length partial sequence at a terminal region thereof exactly matching with the first fixed-length partial sequence defined by the window;

determining whether the second nucleic acid base sequence searched in said moving step and the first nucleic acid base sequence can be assembled or not by comparing a sequence adjacent to said first fixed-length partial sequence of said first nucleic acid base sequence with a sequence adjacent to said second fixed-length partial sequence of the second nucleic acid base sequence to be sufficiently similar via a greedy alignment high speed algorithm; and

assembling said first nucleic acid base sequence and said second nucleic acid bases sequence if the second nucleic acid base sequence and the first nucleic acid base sequence are determined to be assembled.

2. (Previously Presented) A method for assembling nucleic acid base sequences according to claim 1, wherein the nucleic acid base sequence assembled in said assembling step is used as a reconstructed first nucleic acid base sequence to repeatedly carry out said moving, determining, and assembling steps.

3. (Currently Amended) A method for assembling nucleic acid sequences comprising the steps of:

providing a plurality of nucleic acid base sequences;

entering identification information of each of the plurality of nucleic acid base sequences and a respective fixed-length partial sequence located in a terminal region

of each of the nucleic acid base sequences into a table;

constructing a first consensus sequence based on a first nucleic acid base sequence of the plurality of nucleic acid base sequences;

searching for a second nucleic acid base sequence among remaining ones of the plurality of nucleic acid base sequences which has a second fixed-length partial sequence exactly matching with a first partial sequence of said first consensus sequence with reference to said table;

comparing a sequence adjacent to said second fixed-length partial sequence of the second nucleic acid base sequence searched in said searching step with a sequence adjacent to said first fixed-length partial sequence of said first consensus sequence to be sufficiently similar via a ~~greedy alignment~~ high speed algorithm thereby determining the second nucleic acid base sequence can be assembled to said first consensus sequence; and

assembling said second nucleic acid base sequence to said first consensus sequence so as to reconstruct a reconstructed first consensus sequence if the second nucleic acid base sequence is determined to be assembled to the first consensus sequence.

4. (Previously Presented) The method for assembling nucleic acid base sequences according to claim 3, wherein a sequence whose base length is the longest among the plurality of nucleic acid base sequences is selected as said first nucleic acid base sequence.

5. (Currently Amended) A method for assembling nucleic acid base sequences comprising:

a first step of sorting a plurality of nucleic acid base sequences in descending order of sequence lengths;

a second step of entering identification information of each of the plurality of nucleic acid base sequences and a respective pair of fixed-length partial sequences located in a terminal region thereof;

a third step of selecting one of the nucleic acid base sequences whose sequence length is the longest among the plurality of nucleic acid base sequences as a first consensus sequence;

a fourth step of moving a fixed length window along said first consensus sequence to define a first fixed-length partial sequence and simultaneously searching for a second nucleic acid base sequence among remaining ones of the plurality of nucleic acid base sequences which has a second fixed-length partial sequence exactly matching with the first fixed-length partial sequence defined by said fixed length window with reference to said table;

a fifth step of comparing a sequence adjacent to said first fixed-length partial sequence of said first consensus sequence with a sequence adjacent to said second fixed-length partial sequence of the second nucleic acid base sequence searched in said fourth step to be sufficiently similar via a ~~greedy alignment high speed~~ algorithm thereby determining said first consensus sequence and the second nucleic acid base sequence to be assembled; and

a sixth step of assembling the second nucleic acid base sequence searched in said fourth step to said first consensus sequence so as to reconstruct a reconstructed first consensus sequence if said fifth step determines that the sequences are to be assembled,

wherein the fourth step to the sixth step are repeated until said fixed length window completes the scanning throughout said reconstructed first consensus sequence, and said third step to said sixth step are repeated until all of the plurality of nucleic acid base sequences are selected in the third or fourth step and compared in the fifth step.

6. (Currently Amended) The method for assembling nucleic acid base sequences according to claim 3, further comprising a step of ~~specifying a number picking up more than two~~ of said fixed-length partial sequences to be entered into said table for each of the plurality of nucleic acid base sequences.
7. (Previously Presented) The method for assembling nucleic acid base sequences according to claim 3, further comprising a step of designating a range of the terminal region of said first nucleic acid base sequence from which said fixed-length partial sequences to be entered into said table is extracted.
8. (Previously Presented) The method for assembling nucleic acid base sequences

according to claim 3, wherein a base length of said fixed-length partial sequences to be entered into said table is between 10 bases and 32 bases.

9. (Previously Presented) The method for assembling nucleic acid base sequences according to claim 3, further comprising:

a step of specifying an upper limit  $c$  as an expected number of entries retrieved from said table of an identical fixed-length partial sequence located in different nucleic acid base sequences or different positions in the nucleic acid base to be assembled to said first consensus sequences, and

a step of specifying a length  $s$  of fixed-length partial sequences to be entered into said table as an integer satisfying the following expression (1)

$$s \geq \frac{1}{2} \log \frac{KN}{c} \quad \dots (1)$$

where  $N$  is the number of said plurality of nucleic acid base sequences and  $K$  is the number of the fixed-length partial sequences selected from each of the plurality of nucleic acid base sequences.

10. (Cancelled)

11. (Previously Presented) The method for assembling nucleic acid base sequences according to claim 3, wherein each of said fixed-length partial sequences is represented by a fixed number of computing words which are independent of a length of the fixed-length partial sequences.

12. (Currently Amended) The method for assembling nucleic acid base sequences according to claim 3, wherein any entry in said table is removed if a number of entries sharing an identical key therein is more than a previously specified number only entries in said table corresponding to a key, which is the frequency of occurrence of said second fixed length partial sequence in said table, are utilized as said second fixed length partial sequence for searching for said second nucleic acid base sequence.

13-15. (Cancelled)